

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura, Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada, Shigemasa; Takei, Masami

(ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto

(B) STREET: 30 Rockefeller Plaza

(C) CITY: New York

(D) STATE: New York

(E) ZIP: 10112-3801

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

(B) COMPUTER: Compaq PC

(C) OPERATING SYSTEM: Windows 95

(D) SOFTWARE: WordPerfect 8.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/090,672

(B) FILING DATE: 04-JUNE-1998

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/JP97/04468

(B) FILING DATE: 05-DEC-1997

(A) APPLICATION NUMBER: JP-8-325763

(B) FILING DATE: 05-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perry, Lawrence S.

(B) REGISTRATION NUMBER: 31865

(C) REFERENCE/DOCKET NUMBER: 766.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 218-2100

(B) TELEFAX: (212) 218-2200

### (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCTACCGTT TTTCCCTGTC TTTCTATTCC AGGTCAGTCT TCACTGTTTC CG ATG GAA 58

Met Glu

1

GAT GGA TTC TTG GAT GAT GGC CGT GGG GAT CAG CCT CTT CAT AGT GGC 106  
Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly

5

10

15

CTG GGT TCA CCT CAC TGC TTC AGT CAC CAG AAT GGG GAG AGA GTG GAA 154  
Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu

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20	25	30	
CGA TAT TCT CGA AAG GTG TTT GTA GGC GGA TTG CCT CCA GAC ATT GAT			202
Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp			
35	40	45	50
GAA GAT GAG ATC ACA GCT AGT TTT CGT CGC TTT GGC CCT CTG ATT GTG			250
Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val			
55	60	65	
GAT TGG CCT CAT AAA GCT GAG AGC AAA TCC TAT TTT CCT CCT AAA GGC			298
Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly			
70	75	80	
TAT GCA TTC CTG CTG TTT CAA GAT GAA AGC TCT GTG CAG GCT CTC ATT			346
Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile			
85	90	95	
GAT GCA TGC ATT GAA GAA GAT GGA AAA CTC TAC CTT TGT GTA TCA AGT			394
Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser			
100	105	110	
CCC ACT ATC AAG GAT AAG CCA GTC CAG ATT CGG CCT TGG AAT CTC AGT			442
Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser			
115	120	125	130
GAC AGT GAC TTT GTG ATG GAT GGT TCA CAG CCA CTT GAC CCA CGA AAA			490
Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys			
135	140	145	
ACT ATA TTT GTT GGT GGT GTT CCT CGA CCA TTA CGA GCT GTG GAG CTT			538
Thr Ile Phe Val Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu			
150	155	160	
GCG ATG GTA ATG GAT CGG CTA TAC GGA GGT GTG TGC TAC GCT GGG ATT			586
Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile			
165	170	175	
GAT ACC GAC CCT GAG CTA AAA TAC CCA AAA GGA GCT GGG AGA GTT GCG			634
Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala			
180	185	190	
TTC TCT AAT CAA CAG AGT TAC ATA GCT GCT ATC AGT GCC CGC TTT GTT			682
Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val			
195	200	205	210
CAG CTG CAG CAT GGA GAG ATA GAT AAA CGG GTA AGC CTT ATA CTA CAT			730
Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His			
215	220	225	
TTT GGA AAA TTC TAGAAATGGT CCTCTAAATG TGTGATTACC AATATTAGAA			782
Phe Gly Lys Phe			
230			
CGGGAGCATT TTATGACAAT AAAGTGACAG CTGACAATTT TGCCATAGA GTTAATTATG			842
GTCTATAATA CATGAAATAA TGTCTATGA ATTTCTTTA TCTTTCAGTT TTTTGAGTAG			902
CCTAACATCAGA ACACATACAAT TTACTTGAGT TAATTTAACAT TTCTCTAACT TCCATTCAAT			962
CTCAATCCAT CCGTCCATTG ATTCACTTAG TTTGTAAGTC ATTCAATAAAA TATTTACTGA			1022
ATCCTTTGTT CTGTGTTATA TCAAGTATAC AAACAGGAAT GCCCTTGAGG TTTCTGCC			1082
TTTTTTTTGT TTGTTTTTA ATCCTGGGAC ATAGGGAAGA CCTCAGCAAG CCCTATTCT			1142
CAATGAATTG TACTCACAGA TTTCTTTTT TTTTTTTT TCTTTTCCA CAGCCGCCAC			1202
CTCTCACCGA TTATTCCTT AGCTGGTGT TTCATGTATT CAACAAACGT TTTAGTGCTT			1262
AGGGCAAGAA GTTCCGTGCC TCATGAGTTT ATTCCTAGC AGATAGAACT GTATCACTG			1322
CCAGTACTAC TCAGAGTGTG GCCTGTGGAC TGACCTCCAG TCTGTAAACT TAGTTGTAG			1382
TGAGATAGGA ATTTAGACCA GAATGTGTAA TCAACCACAT TACTGGGCAC AATGTTGGT			1442
CCAGCTGGCG ATTTTTTTT CATAGAAAGC CTTTATTGAT GAGGGAAAGCA ATATATTGAT			1502
TTATATTTG GGGTCACCTT TTTATTCAT GGCACACTGG CACTTCATG CATGCTGACT			1562
TTGATATCCA TCACTCTGAG GCATTGTGCT AAAATAGATT GATTTATCG TGTGTTCTC			1622
AATTCAAGAT GTAAAAATCA TCAAGTCAGT AGCAGTTTT GCTTTTATG TTTCATGTCA			1682

TGTACAGTCT	ACTTCACTGG	CAGTAaaaaaa	ATTTAAGATA	GTGGTGGTCA	TCCTACAAAC	1742
TGTGAATCTA	TTAAAGAGAA	AAGTATCTGT	TCTATTCTAA	GCATGGGGGA	GGGACAAGAT	1802
TAGTATGTTA	ACATGCCTAC	TTTGTGTTGTT	TGAGATGGAG	TCTCTCTCCG	TCACCCAGGC	1862
TGGAGTGCAG	TGGTACAGTC	TCAGCTCACT	CCAACCTCTG	CCTCCCGGGT	TCAAGTGATT	1922
CTCCTGCCTT	AGCCTCCCGA	GTAGGTGGAA	TTACAGGCAT	ATACCACCAT	GCCCAACAAA	1982
TGTTTGTATT	TTTAGTGGAG	ACAGGGTTTC	ACCGTGTGTTG	TCAGGCCAGT	TTCAAACCTCC	2042
TGACCTCAAG	GGATCCACCT	GCCTCACCCCC	CTCAAAGTGC	TGGGATTACA	GGCATGAGCC	2102
ACCCACCATG	CCTGGCCTAC	TTGGTTTTTT	ATGCACACTA	AAAAATACCT	ACATCTCACT	2162
GCCTTATTCC	AACATAAGTT	TCAGAGCTGT	GGGATTGGTC	ATTAGAAATT	CAGACTGAAT	2222
TTGTTTCTCT	CTGCAATGAA	ATCCTTGCC	CAGTGTTCAT	GTCACTCTGT	AGACATTATG	2282
GAGCAGCCTA	GAGGCCAGAA	GCCCAGTGT	CTCCTTATGC	CTGCTCTTCC	TGGGCTTCTGT	2342
GACACTCTTC	TTCTCCTTTT	GTACTTTAT	TTTTTAGTT	AAAAAATTTT	TTTTAGAGGG	2402
AGGGTCTCAC	TCTGTCAACC	AGGCTGGAGC	ACAGAACATAC	AATCATGACT	CACTGCATGT	2462
TCTTCTCCTT	TTGTTCATGG	CTAATCTTGG	TCAGGATTCC	TTGTCAGAGC	TGGGTGGCAC	2522
CAGTGCCTGGT	GACAGCCTGC	TGTAAGGGAG	TTTCAGCCAT	GAATCTCTCC	AGACTAAAAAA	2582
TAACCAGCTC	TTTTCTAGCT	GATGAATTAA	TAACCAGGTG	ACTGTTAATG	CTTGAAAGGT	2642
TCACATGACA	GGTTGGCCGA	TAGAACGCTG	GAACAGGCC	AGTTTTAGAA	ATTCACCTCT	2702
GACTTTAGA	CTCAGGTGAA	CCATTCTTAC	TGAGAAAGAA	CAAAGCAGGG	TTTTAGACTG	2762
TGAATCCTAT	GGCTGCATCT	TTTTTTTTT	TTAACAGAG	TTCCAGGTTT	GTGATTATAA	2822
CCCAACATGT	GTACACTATA	AATAGAAACC	ACGAGGCCAGG	CTTTTACGA	CAGCTCAGAA	2882
TCTTGTGACG	CAGTAGTCAG	GCATCTTCAC	ACCGACTTGA	ATATTGAAGT	CGAGTTGTGT	2942
GGAACTTGGA	TCATCTTAGT	TGATTTGTT	TAATTATGA	TTCCACATAT	GACAAAAATC	3002
CAGATCCACT	AATTAAAATG	AGGGTTTATG	TCTATGAATA	ATCTCCTGTG	GGTTTAATCT	3062
CATAACATTC	TAGTCTAAC	AGTTGGCTTC	ACTTCATGAT	GTCTGCTAA	ATCCTTTTC	3122
CTTTAAAGGA	TGTTTATTAA	ATAAGAAAAA	AAATGTAAA	TGATAGATAA	AAAAGCCTT	3182
ACTAGGTTCT	AAAAGATGA	ACTATCCATA	TTTCAGTAAA	TGAATAATT	GTCCCTCCTC	3242
TTTGGGCACC	TTGGAACAGA	TTCAATTAGA	TAGTGGGTGG	AAATGTACAT	GTATGGTAAG	3302
CATTGCTGGC	CTAGTCACTG	AAAAATGTAA	ACTCTTATT	TTGATTGCAG	GTGGAAGTTA	3362
AGCCATATGT	CTTGGATGAT	CAGCTGTGTG	ATGAATGTCA	GGGGGCCCGT	TGTGGGGGGA	3422
AATTGCTCC	ATTTTCTGT	GCTAATGTAA	CCTGTCTGCA	GTATTACTGT	GAATATTGCT	3482
GGGCTGCTAT	CCATTCTCGT	GCTGGCAGGG	AATTCCACAA	GCCCCCTGGTG	AAGGAAGGCG	3542
GTGACCGCCC	TCGGCATATT	TCATTCGCT	GGAACTAAAG	GATAACTGCA	GTGCTCATTT	3602
TCAGGCCTCA	GAATAAGTGC	ACTCTCTGT	TCATTCTGAC	CCCTTCCTCA	ACCTCTTCAC	3662
GCTGGCATGT	CCTTTGTAG	CAGCTGTAA	CTTAACATA	GTATAATGAA	AAGAATGACC	3722
TATAATATAG	GTGTTTGTA	GATTCTGTG	TCACTGCAAA	CAATATGAAC	TCCTTTTCG	3782
TATTGCCATC	GGGTTGCATG	GAAGTTTTAT	TCTCTGTTT	TGCTGGAAAC	CAAGAGGATC	3842
CAAACCTCCT	GCAACATTAA	CTTAGAGGGAG	AGAGAGAAAT	ATTAAGAGAG	AAATGAAACA	3902
ATAGAGTATT	TTGGGTTTT	AATTAAATTAA	TTGTTAATAA	TATAACATAT	AAGAATACTT	3962
TTATTAAGAT	AACCATGCAA	CAATAACACT	ATCGGTCTAT	CTGACAGTTT	TTCCCCCAGG	4022
GAAGTGCTT	TGCCCTTTCC	TTTCTTTTTT	TTTTTTTTTC	ATCTTTTTG	TTCTCTCTCT	4082
TTTTCCATC	CCTTTTTAA	TTTTTAACA	GCAATGGAGG	AAGTTAACAA	TTTTTAATGG	4142
AAAGAGCATG	TTAGAGCAAA	CAAATGCATA	AGCAAGACTG	AGCAGCATT	TAATTAATT	4202
TCAGGGTTT	GAGGCTGAAC	ATAATTCTAT	TATCCCTCAA	AAAGTTACCA	CCACATCAGA	4262
AAAAAAAAAA	AAAAA					4276

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTGGAGGTT	CTGGGGCGCA	GAACCGCTAC	TGCTGCTTCG	GTCTCTCCTT	GGGAAAAAAT	60
AAAATTTGAA	CCTTTGGAG	CTGTGTGCTA	AATCTTCAGT	GGGACA	ATG GGT TCA	115
					Met Gly Ser	
					1	
GAC AAA AGA GTG AGT AGA ACA GAG CGT AGT GGA AGA TAC GGT TCC ATC						163
Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile						
5	10	15				
ATA GAC AGG GAT GAC CGT GAT GAG CGT GAA TCC CGA AGC AGG CGG AGG						211
Ile Asp Arg Asp Asp Arg Asp Glu Arg Ser Arg Ser Arg Arg Arg						
20	25	30	35			
GAC TCA GAT TAC AAA AGA TCT AGT GAT GAT CGG AGG GGT GAT AGA TAT						259
Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr						
40	45	50				
GAT GAC TAC CGA GAC TAT GAC AGT CCA GAG AGA GAG CGT GAA AGA AGG						307
Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg						
55	60	65				
AAC AGT GAC CGA TCC GAA GAT GGC TAC CAT TCA GAT GGT GAC TAT GGT						355
Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly						
70	75	80				
GAG CAC GAC TAT AGG CAT GAC ATC AGT GAC GAG AGG GAG AGC AAG ACC						403
Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr						
85	90	95				
ATC ATG CTG CGC GGC CTT CCC ATC ACC ATC ACA GAG AGC GAT ATT CGA						451
Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg						
100	105	110	115			
GAA ATG ATG GAG TCC TTC GAA GGC CCT CAG CCT GCG GAT GTG AGG CTG						499
Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu						
120	125	130				
ATG AAG AGG AAA ACA GGT GAG AGC TTG CTT AGT TCC TGATATTATT						545
Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser						
135	140					
GTTCTCTTCC CCATTCCCAC CTCAGTCCCT AAAGAACATC CTGATTCCCC CAGTCTCAA						605
GCACATGAAT TCAGAATGAA AGGTTTGCA TGGCTAAGGA ATGTGACTCT TTGAAAACCA						665
TGTTAGCATC TGAGGAACCT TTTAAACTT TGGTTTAGGG ACTTTTTTT CCTTAGGTAA						725
GTAATGATT ATAAACTCCT TTTTTTTTT TTGACTATAG TCGGGTGCAT GGTTACTTTA						785
AGCGTGAAT CAAATGGAGT GGCATTTAGT TCAGGCGGCT TGTTCTTGC CATGGCAAAG						845
TATCAAGAAG ATCCCCAAGT CAAGTCACAT TTGTAAGCT GCTTCCAAT TGGCTTTGTC						905
ACGCAGTGTG GAAGCAGTGG GAGAGAGATT CACCTGTTAT AAAGGAACATG ACTAACACAA						965
GTATCCGTC TATATCTGAA TGCTGTCCT AGGTGTAAGC CGTGGTTCG CCTTCGTGGA						1025
GTTTATCAC TTGCAAGATG CTACCAGCTG GATGGAAGCC AATCAGGTTG CTTCACTCAC						1085
CAAGCTCTAGA TATTCATGAA AATGGAACAA GTCTGTACAA TTTAAAAAA AGGTTGAAGG						1145
AGTGGTTGT TCCAAAGGAG TGACTTTTTT TTAAAAAAA AAGCTTGTA TATATTTAAA						1205
TTGATGTTAC TAGAATAAGT ACAGTACCAA GGACTTCATT ATAGAATTG TTCTGCCTT						1265
AAACATGGCT ACCTACCTGG CAGGGCTTTG TTAACTACTG AATACCTGTC TGGTAATCAC						1325
TAAAACATCT TAATGTTCC CTTTTTCTA GTTTGTTATA TTCCTATTAT GTCCATTGAG						1385
AGTAAGCTTA GTATATCAA CTCTCCATT GACAGTGAAG AGAACATAGT GAAAGTCTGT						1445
GGCGGCATT TTATAAGTAA TTCCCTTATT CTGCCCTGAAG ACCACAAAGC CTCCTGGAGG						1505
CGTAACTGCT CAGACCGGTC TTCAGGGAAT ATTAAAGGAC TTAGTGGAAAT TTATGAACAA						1565
TAAGTCTGAT GAGATTAGCC TGGGAGTGGT GTCCCTGCAGC TGTCTAATCT AGTTAGAGTG						1625
GCATTAACAT TCTAATCTCC TTGAGAATGC CTTTTATAGT CTGTTCAAAG CAAGTCATTG						1685
ATGGTTCTTC GAGGTAGTGT TAACTGAAGT GTTCTTCAGT TTGTCAGAT AATGTTCAAGT						1745
GCTTGGCACT TAAATAACAT TTTTGCAAG AACTCCAAGG CACATTATTG AATGCCTTA						1805
ACCAAGTGCA TTCTGGGAAG TTTGCTTGAC TCATTATCTT GCTTTCTGC AGCATTCTGT						1865
GATTGAGTC ATCCATGAAT CCATGAATAA AAGTTACATT CTTTGATTGG TAATATTGCC						1925

ATTTATAACA	AGACTCACTA	ATGAGGGTAT	CACTTTGACT	GACTGATTG	TTAAAGTTT	1985
TAAGCCTCTC	ATTTCTCAA	CCCAGAAATC	ACAGCCTGAT	TTTATTAAAA	GTAGAGCTTC	2045
ATTCATTTCA	TACCATAGAT	ACCATCCTAG	TAAATCCAGA	ACATATACAA	GGTCATGTG	2105
AGTCTGCTT	CTTGACATGA	TAGCATTGTT	TGATGCAGTG	GATATGTCAG	AATGACTAAC	2165
CTAGGAGTTT	AAAACCTCTA	AGAAACTAAA	ACCTGTAAGA	CATTAAAAG	TCTCCACAAAT	2225
TTTAATGTAT	ACAAAGCTAT	GTTACTGTGT	AAACACATTAC	AGTCAAATT	CACTCCAGAA	2285
ATAAAAGGCC	AGTAGGATTA	GGGACTCACT	GGTAGTTGG	AGTCTCCCAG	CACACATCCC	2345
TCCTAGTGGG	ATGATCTATT	CACATATCTC	CCAGCTTTT	TATTTTGCT	TCTGTATATC	2405
ACAGTGAGTG	GATGGCCCTT	CAGCTTTTC	TCTCCTGGCC	AGACATGCAG	TCTTGCCTT	2465
AGATATCGCA	GAGACAAAAT	TCACAGCATG	TCTTAAATCT	TCCAGGATTT	GCAAGAACCA	2525
AATTGCTCAA	CAGTATGTAT	GTTTAGAGGG	GTTAGACTCC	TTTTAAAAT	CTGGATATCT	2585
AACCACCTAC	TTAAATCTGT	TTGATAGTGT	CAAACCACCC	CCACCCCTGA	TCCTCCCACC	2645
CCCCAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA		2689

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTCTCTCTC	TCTTCACAG	AGTCTTGCTC	TGTCGCCAG	GCTGGAGTGC	AGTGGCACAA	60
TCTCACTGCA	AGCTCCGCCT	CCTGGGTTCA	CGCCATTCTC	CTGCCTCAGC	CTCCCAAATA	120
GCTGGGACAA	CAGGCACCTG	CCACCACGCC	CGGCTAATT	TTTGTATTTT	TAGTAGAGAC	180
AGGGTTTCAC	CATGTTAGCC	AGGATGGTCT	CAATCTCCTG	ACCTCGTGAT	CCACCCGCCT	240
CAGCCTCCCA	AA GTGCTGAG	ATTACAGGTG	TGAGCCACCA	CGCCAGCCA	CATCTTTCTT	300
TCTTCTTT	TGGTTTTGT	TTGTTGTTG	AGACAGGGTC	TTGCTCTGTC	GCCCTGGCTC	360
ACGTGAACCT	CCCACCTCAG	CCTCCCAAGT	AGCTGAGACC	ACAGGTGTGA	GCCACCACTC	420
CTGGGTAATG	TTTGTTATTT	TTTGAGAGA	TGGGGTTTC	CCGTGCTGCC	CAGACTGCTC	480
TCAAACCTCT	GGGCTCAAGT	GATCCACCTG	CCTTGACCTC	CTAAAGTGCT	GGAATTACAG	540
GTGTGAGCCA	CCGTGCTCAG	CCGAGTGTCT	TTCGTATGTT	TTCTGAGCAC	GTGGATTCC	600
ATCTCTCTGC	ATTCTCTGTT	CATCTCAGCC	TGTTTGTTC	ATTGAGATAA	ATGACTTTT	660
CTTGGTAACT	TAGAGTACTT	TGTGTATT	CAGGTTAAC	CCTTATCAAT	TTATATCAGT	720
TGCTGCTATC	TTTTCTTAA	TTTTCTTT	CATTTAAA	ATTACATTGT	TTCAATGAAC	780
AGAATTTTA	AGTTTAACG	TAGTCCACTT	TGTCCATT	CTTTATGACC	GGTGCATT	840
AGGGTCTTGT	TTAAGAAATC	GTTCTTATC	CTGAGGTCA	AAAGATAGTC	TACTGTATT	900
TCTTTAAAGA	GCTGAAAAGG	TGTTTATAT	TTAATTATT	TGGGATTGGC	TTTGTGTGG	960
TGGGGATAAG	GATCACAATT	TTATTCATT	TTTTTCCAC	TTGGTTATGC	CA GTGGCCCC	1020
ATTCCATT	TTTGAATAGT	CTTCTGTGC	AGAAAAGACT	TCACTAGCAG	AGAAGTCC	1080
AGACTTACCC	TTCAAAAGGC	CCCATTCA	AGGCTAGCAC	TTGGCGTGCA	TCTGAGAAC	1140
TGGATTTGG	GGTGGTCTCT	ATAATGTGGT	GTATGCTGAA	CACCCACCTT	TCCTTCTGGG	1200
AGTCTGGAAT	TTGGGTATAT	GTTGGACAGA	GGCTGCCTAA	GTGACCAGCT	TCAACAAACAG	1260
CCCTGGGTGC	TGGGTCACTC	ATGACCCATA	GACAAA	ATG CCA CAC	ATG TTG TCA	1314

Met Pro His Met Leu Ser

1 5

CAG CTT ATT GCT GGA GGA GTT AGC ACA TCC TGT GTG ACT GCA CTG GGA		1362
Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys Val Thr Ala Leu Gly		

10 15 20

GAG GAA ACT GGT GCC TGG TTC CCT GTG TAT TTG TCC CAC GCC TCC AGT		1410
Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu Ser His Ala Ser Ser		

CCC TTT GCT GAT CTC GTT TTT TGT CCT TTT GCT GAG ATA AAT CAC AGC	1458
Pro Phe Ala Asp Leu Val Phe Cys Pro Phe Ala Glu Ile Asn His Ser	
40 45 50	
CAG GAG TAT GAC AAT ATG CGG GGT CCT GTG AGT CCT AAC AAA CAG	1506
Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln	
55 60 65 70	
TTC AAT CTG GGG GTG ATC TTT GGG ATC CCC AAC AAC TGT CGT TTC CCC	1554
Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro	
75 80 85	
ACT GAT AAT AAA ATA ACT GAG AAG CAG CTA TTG GGC AAT GTT CTG AAC	1602
Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn	
90 95 100	
TAC CCT TGAACATTCA TGTCTTCATC TGAACATCCA TCTACTACCC CTGATTTTT	1658
Tyr Pro	
104	
CAGTGCAGGG TGCATATCCT GTATCACCCA ATAAATGGTC ATTGATCACCC ATAGGAAAGG	1718
AACAGTAAA GCTCCACGGT GGTGGAGG AAGGTGGCAG GCATTCAGCG GTAACCTTTT	1778
TGAGCAGATA GATTTTATGT TTTGCAATG AGTGAATAA ATTTTCCCAT ATCTATTAA	1838
GGTTGGCAAT CATTATCTT TTATCATCTT GGAACATTG GAATCCTTT AATATGTTA	1898
GTTAGGAATT TTCTACCTTC CTCATCTTGT CCGATAGTTT AAAATCCCAC AGTTATTCA	1958
CGGGCTCTC ATACCTGCCT GTGTGATTT TAACATGTCA CGCTATGCAA CCAGTTGCTT	2018
TTACTTGTAG AGTGTTCCT TAGGTAATAG CTTATTATTG GTTATGTGAT TACAGTGTGT	2078
TAAAGACAGG TCTGTAGTTA TGTAAAATGC CGTTTCTCTG AGTATCATGG TCATTTCCAC	2138
ATATTCTCT ATTCAATGTAT TTGTAAGAAT ATATCTATT TTGCAGTATT TTATTTATT	2198
ATTTTATTTT ATTTTCTGAA ACGGAGCCTT GTTCTGTCAC CTAGGCTGGA GTGCAGTGGT	2258
GTGATCTCGA CTCACTGTGA CCTCCCCCTC CCAGGTTCAA GCGATTCTCC CGCCTCATCC	2318
TCCCCAAGTCA TTGGGATTAC AGTCACGTGC CATGAAGCCC TGCTAATTT TTGTATTTT	2378
AGTAGAGACA GGATTCACC ATGTTGGCGA TGCTGGTTTC GAACTCCTGG TTTCGAACTC	2438
CTGACCTCAA GTGATCCACC TGCCTCGGCC TCCCAAAGAA CTGGGATTAT GGGCGTGAAC	2498
CACCACGCCA GGTCAAGTTT GCAGTGTGTT AAATACTGTT GTCTTGAGA GGAGAGAGGC	2558
ACGCACATAG ACTATGGTGA TTACCATCAT ATACTGGAAA GTGCAAAGTG TAGCGCAGTT	2618
AACTGTGAGC CATCTCATCA AACCTTAACA GATGTCTCAT TTGTCATCAA AGGGGCTTCT	2678
GTCCCATAGA AATTCAATGTA CCCAACCTAC TCTTCAACCA TGATTTTCT CTGATGGCCT	2738
GTGTGAACAG ATTAATGGTG TCCATCTAAT TCCCTCCCCA CTGGGGAAA GCAAATCATC	2798
AGGCCCATG CAAAAACTGC TCTTGGTTGA GCTTCCTGCC TAAATCATA CCCACAGTGA	2858
ATGGCGTCCC TTATCACCG CTAATGACTC TGACATCTCT CTCCACTCAC ATGTGAGCCT	2918
CCTCAGCTCT CGATAAACAA GTCTGTCTCG GTTCATTAT TCTACAAAAA AAAAAAAA	2978
AAA	2981

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human

- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTCCGGCAC GAGCAGCTTT CTAGTTGGAT TAGGCAACAG AATCCTTGAA AAATGTGTGT	60
GCACAGACCA GGTGGCTCTC TGGGCCAGTG TACTCTGAAA GATGTGTGTC CTGGCCTAGC	120
TGGTTGAGGA AAAGCAGGGC AAGCTCTAGCC AAATCACACA TCTTGAACAG CCCTCATTG	180
TTATACTAAC TTTCACCT TCTGGTGTGT ATAGGAGATA AAGATGGCAG ACGTGCTATT	240
AGGCTGCCAA TGGGAGTGGG CTCTGATATG GTCTTCAAA T ATG AAT CAC CCC TGG	296

	Met	Asn	His	Pro	Trp	
	1				5	
CAT GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA His Val Cys Phe Leu Ph Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro						344
10 15 20						
ATA TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val						392
25 30 35						
TTA AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile						440
40 45 50						
TCA GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser						488
55 60 65						
ACA ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg						536
70 75 80 85						
TTG GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala						584
90 95 100						
GTT GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe						632
105 110 115						
TTT CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						680
120 125 130						
TAAAAAAAAGT CAGCGTGGCA CGTTTTAGTA TGTGTGGCAG ATCTAAASAG ACAATATTAA GATCTCAGGA GTGTTTATTTC TTGAACCATT TTCAAGACTC TAAGATTGAA GAAATAATAA						740
AATATTGACC ATCCTTCAAA GAGAAAAAACAA CAGGGCGATC TTTGGCATAG CCTGTCATT						800
TGCTCACATT TCACTTCTCT CTCTCCAATC TCAGAGCCCC TGCTGTGGAA CAGGTGCTGT						860
GCTGGGTGGC AGGGGAGGTC TCTGGTTTT TTTTTTTTG ATCTCCGTCT TAACATCTAG						920
CCTACTGGAG GAAGTGTATT TAATCATCCA CTTATCTGTT AACATTATC TCTGAGGGCC						980
CGTCACATTC AGAGAAGATT CTAGGTTCTC TACAAGTATC CTCTCACTGT GTACATACTA						1040
AATCAACATC CTGCTGGATT TCCCCCAGAC ATCTCCCTTC ATCACCATTG GAGAGTATCC						1100
TCTAATTGCC AGCCCTATTC ACCATACTCA TCTCATTGAA TCTGGAGTTT TCTGAGAGTG						1160
ACCGGGGGTG GGATGGACAG GATAATTAG CAAGAGTGTAA TAGTAAAAT CTATATAATA						1220
AAAGTTATCT CCCTGTGCC CCCATGATCT ATTCTTTATG TAGCAGTCTG AATGAGATT						1280
TCAGAAACAA GAACCACCTT ACCTTAGTCT CTTCTCTTC TTCTCTTCT TTTCTTTCT						1340
TTTTTTTAG TATTATGGGC AACAGAGCAA GACCCAGTCT CAGGAAAAAA AAAAAAAAAAA						1400
A						1460
						1461

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGGCCCCCG CCAGAATACC CTATCCTTAA ACATGAATTT AGGGGAGGGG AGGACACAAT TCAATCTATA ACAACTATCA CTGGCTGATT	60
TTGGCAGAGG CCTGTGGCCT CCAGTATTGAGGGGAGCTG AGGGCCACTG ATCTCTCCAT	120
	180

ATGCTCTCAA	CATCATGGGA	CTAGTAGGAT	GAAAGCAAGC	CTCAGACCAAG	ATTCTACCTC	240
AAGCAGGCAC	ACAAACATTC	ATGCAGCTTC	TACTTGGAGC	CTGATGAAGT	TCAAATTGTT	300
TGTCCTCTGA	GGCTCTCTT	GCATGGAAAT	TTCTCCCATG	ACAGATGAGA	AAGTTCTGGG	360
GCAGCATTCA	GCTTCTAGT	TGGATTAGGC	AACAGAACATCC	TTTGAAAATG	TCTGTGCACA	420
GACCAGGTGG	CTCTCTGGGC	CAGTGTACTC	TGAAAGATGT	GTGTCCTGGC	CTAGCTGGTT	480
GAGGAAAAGC	AGGGCAAGCC	TAGCCAAATC	ACACATCTG	AACAGCCCTC	ATTCGTTATA	540
CTAACTTCC	CACCCCTCTGG	TGTGTATAGG	AGATAAAAGAT	GGCAGACGTG	CTATTAGGCT	600
GCCAAATGGGA	GTGGGCTCTG	ATATGGCTT	TCAAAT	ATG AAT CAC CCC TGG CAT		654
			Met Asn His Pro Trp His			
			1	5		
GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA ATA					702	
Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro Ile						
10	15	20				
TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT TTA					750	
Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu						
25	30	35				
AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA TCA					798	
Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser						
40	45	50				
GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC ACA					846	
Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr						
55	60	65	70			
ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA TTG					894	
Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu						
75	80	85				
GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT TTT					942	
Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe						
90	95	100				
GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT TTT					990	
Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe						
105	110	115				
CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT TAAAAAA					1041	
His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						
120	125	130				
AAGTCAGCGT	GGCACGTTT	AGTATGTGTG	GCAGATCTAA	AGAGACAATA	TTTGATCTC	1101
AGGAGTGT	TTCTTGAAAC	CATTTTCAGA	ACTCTAACAT	TTGAGAAATA	ATAAAAATATT	1161
GACCATCCTT	CAAAGAGAAA	AACACAGGGC	GATCTTGGC	ATAGCCTGTC	ATTTGCTCA	1221
CATTCACTT	CTCTCTCTCC	AACTTCAGAG	CCCCCTGCTGT	GGAACAGGTG	CTGTGCTGGG	1281
TGGCAGGGGA	GGTCTCTGGC	TTTTTTTTT	TGATCTCCGT	CTTAACATCT	AGCCTACTGG	1341
AGGAAGTGT	TTTAATCATC	CACTTATCTG	TTAACAAATTA	TCTCTGAGGG	CCCAGTCACAT	1401
TCAGAGAAGA	TTCTAGGGTC	TCTACAAGTA	TCCTCTCACT	GTGTACATAC	TAAATCAACA	1461
TCCTGCTGGA	TTTCCCCCAG	ACATCTCCCT	TCATCACCAT	TGGAGAGTAT	CCTCTAATTG	1521
CCAGCCCTAT	TCACCATACT	CATCTCATTT	GATCTGGAGT	TTCTGAGAG	TGACCGGGGG	1581
TGGGATGGAC	AGGATAATT	AGCAAGAGTG	TATAAGTAA	ATCTATATAA	AAAAAGTTAT	1641
CTCCCTGTGC	CCCCCATGAT	CTATTCTTTA	TGTAGCAGTC	TGAATGAGAT	TTTCAGAAAC	1701
AAGAACCACT	TTACCTTAGT	CTCTTCTTCT	TCTTCTTCTT	CTTTCTTTT	CTTTTTTTT	1761
AGTATTATGG	GGATCTGTT	CTGGTGCCCA	GGGTGGAGTG	CAGTGGTATG	ATCTTGGCTC	1821
ACAGCAGCCT	TGAACCTCCG	GGCTCAAGTG	GTCCCTCTGC	CTCTGCTTCC	CTAGTAGCTA	1881
GGACTGCAGG	TTTGTGCCAC	CACACCTGGC	TAATTGAAAA	AAGAAATTTT	TTTCAATAG	1941
AGACAGTGTC	TTGCTATGTC	CCCAGGCTGG	TCTCAAACTC	CTGGCCTCAA	GTGATCCTCC	2001
TGTCTCATCC	TCCCCAAAGTG	TTGGAATTAC	AGGTGTGAGC	TACTATACTC	GGCCAGTACC	2061
CTTCTCAAAA	CACTTCAGCA	CTTCCCATTG	CACTTGGGTT	GAAATTCCCA	CCACTCACTG	2121
GGGCCCACAA	GAACCTTCAA	GAACGAAATCC	TTGCTCAACA	TTGTCAGCTG	CCCCCTACCA	2181
CCTGCAGCCT	CACTTGCTGT	GCTCCAGCCA	TGTGGATCTT	CCTCCTGTCT	CTAAAACACTGC	2241
CTCAGGTCA	TTGCACCTGC	TGTTCTTCCC	AAAGGCTGTG	TGATTTCCAT	CAAGTCAGTCT	2301

TAGCTCGTAT	ACCTCCTTGG	AGACACCTCT	TCTGACCAAC	CAGTCCAAAG	AATCTCCCT	2361
TATCATGTCA	CTCTGTTTA	TTTATTTATT	TAGAGATGGA	GTCTCGCTCT	GTCACCCAGG	2421
CTGGAGTGCA	GTGGCGCGAT	CTCTGCTCAC	TGCAAGCTCC	ACCTCCTGGG	TTCATGCCGT	2481
TCTCCTGCCT	CAGCCTCCTG	AGTAACCTGGG	ACTATGGGCA	CCCACCACTA	CACCCGGCTA	2541
ATTTTTGTA	TTTTTAGTGG	GGATGGGGTT	TCACTGTGTT	AGCCAGGATG	GTCTTGATCT	2601
CCTGACCTTG	TGATCTGCCT	GCCTCCACCT	CCCAAAGTGT	TTTATTTATT	TTAAAGGCAT	2661
GTATCACTCT	CTGAAAATTA	GCTTCTTTCT	TCTTTTCCT	TGTTATCATC	CATTTCCCCG	2721
AACCAGAATA	GAAGTTCTG	AGGCCAGAAC	TTCTGTCTCT	CTGCCCTCA	CTATGTGTCT	2781
CTGGCACATA	CCCCAGTGC	TGCCTGCTCT	AAAGTAAAAT	CTTAGTAAAT	ATTACTGTTG	2841
ACTAAATAAA	TGAATAAATC	CCTTTTAATG	CCCCTTGGG	AGTTGCCAAG	TAAAGAATAG	2901
GATCCCTTT	TAAGATTACA	CTTTGGCTA	TTGATCTGTG	TGTCTGGAAC	AAGATAACAGT	2961
TTGAAGATAC	TACCATGGG	CATGACATCA	GTTGAGCTGA	TTAAGGTTT	AGTAATAAGA	3021
ATCCAGGATG	TGTCCGGGT	CGGTGCTCAC	GCCTGTAATC	CTAGCATT	GGGAGACCGA	3081
GGCGGGCAGA	TCACGAGGTC	AGCAGTTGA	GACCAGCCTG	ACCAACATGG	TGAAACCCCG	3141
TCTCTACTAA	AAAATACAGA	AATTAGCCGG	GTGTGGTGGT	GTCCACCTGT	AGTCCTAGCT	3201
ACTCAGGAGG	CTGGGGCAGG	AGAATTCTT	GAACCCGGG	GGCGGAGGTT	GCAGTGAGCC	3261
GAGATCACAC	CAGTGCAC	TG	AAACAGAGCAA	GACCCAGTCT	CAGGAAAAAA	3321
AAAAAAAAA						3329

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGAACTGGG	AGTCAGGTGG	TTGACTTGTG	CCTGGCTGCA	GTAGCAGCGG	CATCTCCCT	60
GCACAGTTCT	CCTCCTCGGC	CTGCCCAAGA	GTCCACCAGG	CC	ATG GAC GCA GTG	114
					Met Asp Ala Val	
					1	
GCT GTG TAT CAT GGC AAA ATC AGC AGG GAA ACC GGC GAG AAG CTC CTG						162
Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly Glu Lys Leu Leu						
5	10	15	20			
CTT GCC ACT GGG CTG GAT GGC AGC TAT TTG CTG AGG GAC AGC GAG AGC						210
Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg Asp Ser Glu Ser						
25	30	35				
GTG CCA GGC GTG TAC TGC CTA TGT GTG CTG TAT CAC GGT TAC ATT TAT						258
Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His Gly Tyr Ile Tyr						
40	45	50				
ACA TAC CGA GTG TCC CAG ACA GAA ACA GGT TCT TGG AGT GCT GAG ACA						306
Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp Ser Ala Glu Thr						
55	60	65				
GCA CCT GGG GTA CAT AAA AGA TAT TTC CGG AAA ATA AAA AAT CTC ATT						354
Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile Lys Asn Leu Ile						
70	75	80				
TCA GCA TTT CAG AAG CCA GAT CAA GGC ATT GTA ATA CCT CTG CAG TAT						402
Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile Pro Leu Gln Tyr						
85	90	95	100			
CCA GTT GAG AAG AAG TCC TCA GCT AGA AGT ACA CAA GGT ACT ACA GGG						450
Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln Gly Thr Thr Gly						
105	110	115				

ATA AGA GAA GAT CCT GAT GTC TGC AAA GCC CCA TGAAGAAAAA	496
Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro	
120	125
TAAAACACCT TGTACTTTAT TTTCTATAAT TTAAATATAT GCTAAGTCTT ATATATTGTA	556
GATAATACAG TTCGGTGAGC TACAAATGCA TTTCTAAAGC CATTGTAGTC CTGTAATGGA	616
AGCATCTAGC ATGTCGTCAA AGCTGAAATG GACTTTGTA CATAGTGAGG AGCTTGAAA	676
CGAGGATTGG GAAAAGTAAT TCCGTAGTT ATTTCAGTT ATTATATTAA CAAATGGAA	736
ACAAAAGGAT AATGAATACT TTATAAAGGA TTAATGTCAA TTCTGCCAA ATATAAATAA	796
AAATAATCCT CAGTTTTGT GAAAAGCTCC ATTTTAGTG AAATATTATT TTATAGCTAC	856
TAATTTAAA ATGTCCTGCT TGATTGTATG GTGGGAAGTT GGCTGGTGTGTC CCTTGTCTT	916
GCCAAGTTCT CCACTAGCTA TGGTGTCTA GGCTCTTTG GGATTTTGA AGCTGTATAC	976
TGTGTCTAA ACAAAAGCACT AAACAAAGAG TGAAGGATT ATGTTAATT CTGAAAGCAA	1036
CCTCTTGCC TAGTGTCTG ATATTGGACA GTAAAATCCA CAGACCAACC TGGAGTTGAA	1096
AATCTTATAA TTAAAATAT GCTCTAACAA TGTTTATCGT ATTTGATGCT ACAGGATTTG	1156
AAATTGTATT ACAAAATCCAA TGAAATGAGT TTTTCTTTC ATTTACCTCT GCCCCAGTTG	1216
TTTCTACTAC ATGGAAGACC TCATTTGAA GGGAAATTTC AGCAGCTGCA GCTCATGAGT	1276
AACTGATTTG TAACAAGCCT CCTTTTAAAG TAACCCCTACA AAACCACTGG AAAGTTTATG	1336
GTTGTATTAT TTTTTAAAAA AATCCCAAGT GATTGAAACT TACACGAGAT ACAGAATTTC	1396
ATGCGGCATT TTCTCTCAC ATTATATTT TTGTGATTTT GTGATTGATT ATATGTCACT	1456
TTGCTACAGG GCTCACAGAA TTCATTCACT CAACAAACAT AATAGGGCGC TGAGGGCATA	1516
GAAGTAAAAA CACCTGGTCC CTGCTCTCG TTCACTGCT TGTTGGACGA GAAAACAATA	1576
ACGATAAAAG ACAGTGAAG AAAATAACGA TAAAAGACAG TGAAAGAAAA TAACAATAAA	1636
AGACAAGGAA AAAATAACAA TGAAAGTTGA TAAGTACATG ATAAGCGAGG TTCCCCGTGT	1696
GTAGGTAGAT CTGGTCTTA GAGGCAGATA GATAGGTCA TGCAAATACT CTGGTCCATG	1756
GGCCATATGA AAAGGCTAAG CTTCACTGTA AAATAATAAC TGGGAATTCT GGGTTGTGTA	1816
TGGGTGTTGG TGAACCTGGT TTAAATTAGT GAACTGCTGA GAGACAGAGC TATTCTCCAT	1876
GTACTGGCAA GACCTGATTT CTGAGCATTG AATATGGATG CCGTGGGAGT ACAAAAGTGG	1936
AGTGTGGCCT GAGTAATGCA TTATGGGTGG TTTACCATT CTTGAGGTAA AAGCATCACA	1996
TGAACTTGTAA AGGAATTAA AAAATCCTAC TTTCATAATA AGTTGCATAG GTTTAATAAT	2056
TTTAATTAT ATGGCTTGAG TTAAATTGT AATAGGCGTA ACTAATTTC ACTCTATAAT	2116
GTGTTCATTC TGGAAATAATC CTAACACATAT GAATTATGTT TGCATGTTCA CTTCCAAGAG	2176
CCTTTTTTG AAAAAAAGCT TTGTTGAAT CATCAAGTCT TTCACATTAA AATAAAAGTGT	2236
TTGAAAGCTT TATTTAAAAA AAAAAAAAAA AAAAAAAAAA	2276

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAAA ATGTTAGGGC TTAATATTAT TCATAGATCG AGGATAGTTT CATTCTTAGT	60
CGCCTCTTA GTCACTCTTC CTATACCAAT CTGAGACCAT TTTACAATTG AGAAAAGACA	120
AATAACTGGT TGGGTTACTT GATAGTATAA TAACC	155

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
(vi) ORIGINAL SOURCE:

(A) ORGANISM: human  
(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60  
GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120  
AGGTCCATCC AGAAAATTGGC TTCAAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180  
CAGAGCCGGA GACATTTGTC AGCCAACGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240  
AGTGAACAG GAGATTAGA AGCGTTAGAG GGAAAGGA 278

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human  
(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCTGACAAT GAGTAAGAAG AAAGAGGGTC TTGCCCTTG GTTATTAAGA TTTATCATAG 60  
AGCAATAATA ASTAAATCGG TGTTATACCA GCACAGAGAT TAGACAAATA AACCAAGGGA 120  
CTGGACTAAA TAAGC 135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human  
(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGTACCCA GTTTCAAATT AACATGGTTA TTTTACTTGT GTTCCCAAAT TTAACATTAG 60  
GGAATTTTG GTTGTGGTC TGTTATCACT AGAAAAATAT ATATATTGGT GCTGAAGATA 120  
ATTTGAGAT AATTAGACAA GACAGTTAG CATTACAAAG AACAAAGTTG GCAGTTGAAG 180  
AATCTATTAA TATGACT 197

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human  
(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCGCACC TGGCTGATGC TTTCTATCT GACTCTTTC AGAGGACCCCT GAAAGACACT 60  
AAGTGGAAATC TTTCCTTGAA GTCTCCAAG CTAAAACAAT TCTCTGGAAA GATCACCTCT 120

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
CGTTTACAGA TTCTCTTGC GCTGGCGGTG GAACTACAAA GGGATCGGTG CCTATATCAC 60
AATACCAAA AC TTGATAATAA TCTAGATTCT GTGTYTCTGC TTATAGACCA TGTTTGTAGT 120
AGTAAGAGG AAAACTCCT ATATTCTGAA ACAGCCTAAC ATTTACAAA ATTTAGTTT 180
TCTTTTTAG AGTCTTATCC TGTAGCTATA TAACAGTCA TGTCTGATT AGCATTGTT 240
CACGAGTAAA GCTGGAACTA TGAAAATTGA AAAT 274
```

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GATTAGGTGA CCTTCCTTGA ARAGCCACGG GTTTCCCATA TCGAAATGCT ATTCAATTACC 60
CGAGTCACCT ANGTTCTTAC AAAGGAAGCG AGAAAATTGC TTTTGTGTTGGG CCATGCCCT 120
TTGCANAGG TTCCTAAGTA TAGTCGCCAN AATTTTTTA ATGGCCTAAA G 171
```

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
AGGGCGCTT GTTCTGCTCT CAGCAGATTG GTTACACGCG TCAGGTGGTG GCGATGACTT 60
AATTCCTAGC CCAAGAAGAA TATAATGTTA AAACCTGGTTA TGTAATTTT GTGCCTCTCC 120
TTTTAATGC AGTATTTAGT TCAGATGTT GCGATTTTC A 161
```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATAAGGWGG GAACCTTAATC ATCTCTAATG ACCTTACTGA TGCTGACTTT AATACTCTGT 60  
GAAGGTTAGA GTTCAGTCAA TGTTACCTAG AAACAGCCCC GGCTGTGGAA TACTTTATTG 120  
TTAGCCCTAT ATTTGGGTT TGGATGTCCA CTGTGCTGGT TCCCAGAGAT AGTAAGGGGA 180  
TGAGAGTATT GGTTACATCT CCTGACCCAC ATACTTAAGA TCCAGATGAA CAAGACAGTT 240  
TTCACTCCTG CTTGGTAGAA CCTATTGYK SHAGGAAACA GYTCCCTAAAG AATGGTTCTA 300  
GCCAGACCCCT GTCGYTACCA GAA 323

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGTATGACAA ATAGTTCTG CCTGATTGGT GAGATTTGGG ATGGGGCCCC ACTTTGTTTC 60  
TCTTTCTGCA TAAAAAATTC AACATTTTA CAAAATTTTC AAAAACTTCT CCTCAGTCTG 120  
TACATCTTTG TTAATCAG 138

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGATCCCCAC AATTCTTGT GATTGGTAG GAACTATAAA TGACTCCCAT CCAAGCTTAT 60  
ACCAAGAAAAA AGGAGCACAT TTTCTACAAA TTATATCATT TTTAACCCAT TACCACATTA 120  
TTTTAGGGGA ACTAC 135

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGAGAGGAG CCATGTATAAC AAACCACCTT TTCTAACATG GTCTTTATTA AACTTTGAAT 60  
ATAAGTACAC CTGCTCGAAG TGTCATCTA TATTATTTAA GAACAAGCAA CTGTAAAACA 120

GTAAAATCAC AAAAGGTAAG TTGTTGGAAG ACAACAAAAA AGAATTACTA TATCTGATCC 180  
TGCCTGTTA TTTAGAAC TGTTAATAGG CCTACAGCT 219

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACAGTGAGTG TGGCTGAAAC CTAAGCTGAA GGAAGGGAGG AGCAGGCCACT GCCATGAGGG 60  
GTCCCCTGGAC AGAAACTCTT CAGCAGGCCT TGAAGTTAG TTCAGGGGCT ACATGGAATA 120  
CCACTATTAA GCACACAGGT GTGATCTGAG GTGAGGGACT ACCTTTCGA TCTTGGTTTT 180  
CTCATTATT T 191

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGAGGTGA AGGGAAAGGAA AGAAAGGAAA AACTATCTAC CTGGCAGGAA AAGAGATAAG 60  
CTCCCAAGAA CACCAAAGCA GATGATGAGT CTAGCTCTAC CCAGCCTTCC TCCCCACGAA 120  
TCCAGATCAT AGTAAGAAAC TCTGGGCT 148

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACCACCAAG AAATGAACAA AAAGCATTTC ACCTAAAAAT ACACCAACAA AATGTACTCA 60  
GCTTCAATCA CAAATACGAC TGCTTAAAC CGCAGAAATT TCCTCAACAC TCAGCCTTAA 120  
TCACTCAGCT GGATTTTC CTTCAACAAT CACTACTCCA AGCATTGGGG AACACAACCTT 180  
TTAACATCAC TCCAGTCGTT TCACAATGCA TTCTAATAGC AGCAGGATCA GAACAGTACT 240  
GCATTTACTT GCCAACAGAA CAGACAGACC TGAAGTCAAG ACAACTGCAT TCTCTGTGAA 300  
GTCTGT 306

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTAGCATTTC GGCAGAACCA TTGTTAATTA AAGGGACTTY TGGACCGCAA CYTTAATGTA 60  
CCAGATTATT GAGCRGCCCCA ATGAATGCTT CATTCTCATT GTTTAAGGTG CTGCTTTGAT 120  
TTTTTTCA ATTCTTGTA CTATTTTTA TTTTTGGAG AGGCACATCC CCAAATTG 180  
ATGAGGTATT TGTTGATAAA TAATTCATCA ATTTCCACAA TGCAACACAA AATGTCTGCC 240  
CAGAGTGGAA AAATAAAACA AGGGGGAGAA GAGTTGAGT AACGGAGAAG TTCTGTGGAA 300  
TCCTAGTGAC AAAAGTTGAG AACTACCTT TAAATAAGAC AGTGAAGTAA CAAATGT 357

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGAATAGGCC AGGAGAACCC TGGAAAAGTA GAATAATGAG GTAGGGCTTC CCTTCGCTAT 60  
TTTGAAGTGC AGATTACACT ATGTAAAACC ATTAGGAACCT GGCACGTGAA TAGACAGATC 120  
AATAGTTAAT AGCTGTATTA GCCAGAAAAT GGTGTAAGGA CAACAGGCTA ACTAACCCCTG 180  
TCACTTGTTA TGCTAAAATT AAGTCTAGAT AGAGTCCTC 219

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGAAAGGGGA ATAGAACGCAC AAGAGTCAGT AATCAATAAC AAACAACCTCA AGGTGCTCCT 60  
TCCTTACACT GGTGTTCCCC AAAGTGAGGT GAATTGCCAG CCACCTGGGAG TCAGGGCCAG 120  
TTACATAAGA CATTCTCGGT AAGCCCCCTT TGGGTATCCC AAATAAGGAC TGGGGTGGGT 180  
TTATGTGTAG TCCATTATTA ACAACTAACAC GAACAAACCT AGTGAATTGC AATAAATTCA 240  
CACCAACAGA A 251

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTTGAAAGAG TCCTTGGAAAG GCTTTAGAC CAAACCCCTC TGCATGCTCA ARCCTTGGGT 60  
ACAGGATTTC TAAGAAGTGG AACAGTCTCC AGGGGTGTGG ARCTCATCGC TCAAGGCAGG 120  
TTATCTTATC TGAATAATTT TGTCTGTTGA CTATTGGAT AGTTCTCCTT CAGATGAGCT 180  
GAAATTTCCT CCATAGCTTC CTCTATTAAA CCCAATTCCA CTTCTCAGGG TCA 233

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAAAGCGCT GAAGTTAACGC ATTAATACGC CAGATTCAATG ATTTATGATC AGTATCCAAA 60  
ACTCCAACTA CAAACAATGC AAAGTAGTGC TCCTCAGTAT TATTTTGCA ATTGTTAGTA 120  
ATGTTAACGA TCAAGGAAAA TAAAACACAT CATTGCACAT TACAGCCGCA AAAAAC 176

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGAGAGTAAA GCAAGCTATT TTGACAGCAA CCTAATAACA GCTGTCTTCT TCCACTTCTT 60  
GGCTAACTCA TCCCCCAGAT AGCCTTCTTT TCTCTTATCA ATTCCCTGTT GCAACAATAA 120  
TAAATGCCAC ACCTGATGGA GTCATTAGGC ACTTCCCTAG TGACAAGTGC CTAGGACAGA 180  
GGAGAAAACA AAGAACACT GACAACCCT GAAAACGTAC ATATCAGGCC AGGCATGTCA 240  
C 241

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCTGGAGAGG TGGTGATGTT GCTGAATAAT TGCTTTTAA AGCTGGAGGG GACTTCCAAG 60  
AGTCTCTCAT TTAAGAARAA AAATTAAGA CATAATTGGT AACGGTTTG ACTGCTGCAG 120  
AGGCAACACT TTGCTCACAA TCCTACAGAT CTACTTCACC TGTAACATCA ATTTCTG 180

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AATCTTAGCA TAATGCTTCC	TGGGAAATTTC	TGAAATTGAT	TCCATTCTG	CCGTTACAAA	60
CACACACGAA GTTCCTAGTT	CACTGGGACT	TCCTGATTG	TTCTTTAGC	TTGCTCCTTC	120
TCACCTAGAA GCTCTGTTTA	TTTCTGAGCA	ACCCCTGGGGC	TTGTCTCAT	GGACAGGATT	180
TATTTATCTC ATCAAGGCTG	AGTGTGCCTT	AGGAAGTCAT	AAACATAAAA	AGA	233

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TATAGACAGG GTAGGGACGA TTAGCCCCTC	GACAACCTTT	CACAAATATA	CACACGTTA	60	
ACTACCTCTC AGGTCTATGAT	AAAGACCGGC	CGGGCAGAAA	CACTGTAATC	CCAGCTACTC	120
GGGAGCCTGA GGCACTGAGAA	TCACTTGAAAC	CTGGGAGGTG	GAGGTTGCCA	TGAGCCGAGA	180
TCACGCCATT GCACTACAGC	CTTGGCGACA	AGAGTGAAAC	TCCATCTG		228

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCTTATGATT ACAAAACATCC CTCATATGAA	AATCTCAGCA	TTTNCTGGCT	GCTGCCTTCA	60	
ATCGCTTTTT CTGAAATAGG TATCCCTTGA	TGTCGACTAT	TTGATTCAG	CCAGTCGTTT	120	
CTCTCTGGCA GTGCTCCCTG	CAAATGTGTC	CTTCAAGAA	AACAAAACCT	GCAAGTGGCT	180
TGTAATGTAC CATGACCTTA TCATGTGAAG	GACAAATGGC	TCTTGTCCTT	ATTAGATAGC	240	
AGATGAACTG ATGAACTGAA TTCTGGTCT	GAAGCTTGA	TAAGGTCAGA	TGTCTTTG		298

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(i) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACTTCGAAGG GAAAAAGAGG AAGGAAAAGG ACTGTTAATA AAATAACAAA GGCAGCAATC 60  
AGAACATGAACC AGAGCCAGGA CAGCGTAAAG GCTAGGTTCA CAGTGAGATG AAAGAACCTG 120  
AAAAACAAGTT TAAAACCTCAA AAGAGGGATTA TTCTCAAGTT ATACTACAGT GAAAAAAACAT 180  
GGAAAAAACAC AAAAAGGACA GGCAATAAGG CACAGGCATA CATAACAAGGC AAATTGTAAC 240  
ACAATATTAA CTTGCAAAAG AGCCACAGA GACATGTCAA TGAAGTCATA G 291

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His  
1 5 10 15  
Ser Gly Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg  
20 25 30  
Val Glu Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp  
35 40 45  
Ile Asp Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu  
50 55 60  
Ile Val Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro  
65 70 75 80  
Lys Gly Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala  
85 90 95  
Leu Ile Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val  
100 105 110  
Ser Ser Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn  
115 120 125  
Leu Ser Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro  
130 135 140  
Arg Lys Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val  
145 150 155 160  
Glu Leu Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala  
165 170 175  
Gly Ile Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg  
180 185 190  
Val Ala Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg  
195 200 205  
Phe Val Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile  
210 215 220  
Leu His Phe Gly Lys Phe  
225 230

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Gly	Ser	Asp	Lys	Arg	Val	Ser	Arg	Thr	Glu	Arg	Ser	Gly	Arg	Tyr
1									5			10			15
Gly	Ser	Ile	Ile	Asp	Arg	Asp	Asp	Arg	Asp	Glu	Arg	Glu	Ser	Arg	Ser
									20			25			30
Arg	Arg	Arg	Asp	Ser	Asp	Tyr	Lys	Arg	Ser	Ser	Asp	Asp	Arg	Arg	Gly
							35		40			45			
Asp	Arg	Tyr	Asp	Asp	Tyr	Arg	Asp	Tyr	Asp	Ser	Pro	Glu	Arg	Glu	Arg
							50		55			60			
Glu	Arg	Arg	Asn	Ser	Asp	Arg	Ser	Glu	Asp	Gly	Tyr	His	Ser	Asp	Gly
							65		70			75			80
Asp	Tyr	Gly	Glu	His	Asp	Tyr	Arg	His	Asp	Ile	Ser	Asp	Glu	Arg	Glu
							85		90			95			
Ser	Lys	Thr	Ile	Met	Leu	Arg	Gly	Leu	Pro	Ile	Thr	Ile	Thr	Glu	Ser
							100		105			110			
Asp	Ile	Arg	Glu	Met	Met	Glu	Ser	Phe	Glu	Gly	Pro	Gln	Pro	Ala	Asp
							115		120			125			
Val	Arg	Leu	Met	Lys	Arg	Lys	Thr	Gly	Glu	Ser	Leu	Leu	Ser	Ser	
							130		135			140			143

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Pro	His	Met	Leu	Ser	Gln	Leu	Ile	Ala	Gly	Gly	Val	Ser	Thr	Ser
1										5		10			15
Cys	Val	Thr	Ala	Leu	Gly	Glu	Glu	Thr	Gly	Ala	Trp	Phe	Pro	Val	Tyr
								20		25		30			
Leu	Ser	His	Ala	Ser	Ser	Pro	Phe	Ala	Asp	Leu	Val	Phe	Cys	Pro	Phe
							35		40			45			
Ala	Glu	Ile	Asn	His	Ser	Gln	Glu	Tyr	Asp	Asn	Met	Arg	Gly	Pro	Val
							50		55			60			
Ser	Pro	Pro	Asn	Lys	Gln	Phe	Asn	Leu	Gly	Val	Ile	Phe	Gly	Ile	Pro
							65		70			75			80
Asn	Asn	Cys	Arg	Phe	Pro	Thr	Asp	Asn	Lys	Ile	Thr	Glu	Lys	Gln	Leu
							85		90			95			
Leu	Gly	Asn	Val	Leu	Asn	Tyr	Pro								
							100								

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
1 5 10 15  
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
20 25 30  
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
35 40 45  
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
50 55 60  
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
65 70 75 80  
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
85 90 95  
Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
100 105 110  
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
115 120 125  
Thr Arg Thr Asp Ile  
130

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
1 5 10 15  
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
20 25 30  
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
35 40 45  
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
50 55 60  
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
65 70 75 80  
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
85 90 95  
Ser Leu Glu Pro Ala Phe Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
100 105 110  
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
115 120 125  
Thr Arg Thr Asp Ile  
130

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly  
1 5 10 15  
Glu Lys Leu Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg  
20 25 30  
Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His  
35 40 45  
Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp  
50 55 60  
Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile  
65 70 75 80  
Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile  
85 90 95  
Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln  
100 105 110  
Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATGAAGTG AAGCCAAGTG TTTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT	60
ATTCATAGAC ATAAACCCCTC ATTTAATTA GTGGATCTGG ATTTTGTCATGTGGAT	120
CATAATTAA ACAAAATCAA CTAAGATGAT CCAAGTTCCA CACAATGCA CTTCAATATT	180
CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCACAAAGAT TCTGAGCTGT CGTAAAAAGC	240
CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTTGGGT TATAATCACA AACCTGGAAC	300
TCTGT	305

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAAACCACGG CTTACACCTA GAGACAGCAT TCAGATATAG ACGGGATACT TGTGTTAGTC	60
AGTCCCTTTA TAACAGGTGA ATCTCTCTCC CACTGCTTCA ACAC TGCGTG ACAAAAGCCA	120
TTGGGAAGCA GCTTTACAAA TGTGACTTGA CTTGGGGATC TTCTTGATAC TTTGCCATGG	180
CAAGGAACAA GCCGCCTGAA CTAAATGCCA CTCCATTGA TTCCACGCTT AAAGTAACCA	240
TGCAACCGAC TATAGT	256

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TACTCTTCAA CCATGATTT TCTCTGATGG CCTGTGTGAA CAGATTAATG GTGTCCATCT	60
AATTCCTTCC CCACTGGGG AAAGCAAATC ATCAGGCCA TTGCAAAAAC TGCTCTGGT	120
TGAGCTTCCT GCCTTAAATC ATACCCACAG TGAATGGCGT CCCTTTATCA CCGCTAATGA	180
CTCTGACATC TCTCTCCACT CACATGTGAG CCTCCTCAGC TCTCGANAAA CAAGTCNGTC	240
TCGG	244

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCAGAAAA CTCCAGATCA AATGAGATGA GTATGGTGNN NAGGGCTGGC ATTAGAGGA	60
TACTCTCCAA TGGTGATGAA GGGAGATGTC TGGGGGAAAT CCAGCAGGAT GTTGATTTAG	120
TATGTACACA GTGAGAGGAT ACTTGTAGAG AACCTAGAAT CTTCTCTGAA TGTGACGGGC	180
CCTCAGAGAT AATTGTTAAC AGATAAGTGG ATGATTAAT ACAC TTCCCTC CAGTAGGCTA	240
GATGTTAAGA CGGAGATC	258

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid; synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGCTTAATA TTATTCATAG ATCGAG	26
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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
GTTATTATAC TATCAAGTAA CCCAAC

26

(2) INFORMATION FOR SEQ ID NO:45:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:  
GTGGATCTGG ATTTTTGTCA TATGT

25

(2) INFORMATION FOR SEQ ID NO:46:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
GTTTGTGATT ATAACCCAAC ATGTG

25

(2) INFORMATION FOR SEQ ID NO:47:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
GAAGGGGAAG AGACATTAAG TTATC

25

(2) INFORMATION FOR SEQ ID NO:48:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
GCTTCTAAAT CTCCTGAGTC ACTT

24

(2) INFORMATION FOR SEQ ID NO:49:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
GACAATGAGT AAGAAGAAAG AGGG

24

(2) INFORMATION FOR SEQ ID NO:50:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:  
GTCCAGTCCC TTGGTTTATT TGTC

24

(2) INFORMATION FOR SEQ ID NO:51:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:  
GGTACCCAGT TTCAAATTA CATGG

25

(2) INFORMATION FOR SEQ ID NO:52:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:  
GATTCTTCAA CTGCCAAACT TGTTC

25

(2) INFORMATION FOR SEQ ID NO:53:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:  
GCTGATGCTT TTCTATCTGA CTTC

24

(2) INFORMATION FOR SEQ ID NO:54:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:  
GACCAGGACT GAACAGAGGT GA

22

(2) INFORMATION FOR SEQ ID NO:55:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
GCTTATAGAC CATGTTTGTA GTAGG 25

(2) INFORMATION FOR SEQ ID NO:56:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
GTGAACAAAT GCTAAATCAG ACATG 25

(2) INFORMATION FOR SEQ ID NO:57:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:  
GCCACGGGTT TCCCATATCG AA 22

(2) INFORMATION FOR SEQ ID NO:58:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:  
GACTATACTT AGGAACCTCT GCAA 24

(2) INFORMATION FOR SEQ ID NO:59:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
GTTCTGCTCT CAGCAGATTG GTTA 24

(2) INFORMATION FOR SEQ ID NO:60:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
GCCAACATCT GAACTAAATA CTGC 24

(2) INFORMATION FOR SEQ ID NO:61:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:  
GTTCAGTGAA TGTTACCTAG AAACA 25

(2) INFORMATION FOR SEQ ID NO:62:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  
GGAGTGAAAA CTGTCTTGTGTT CATC 24

(2) INFORMATION FOR SEQ ID NO:63:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
GTATGACAAA TAGTTCTGC CTGAT 25

(2) INFORMATION FOR SEQ ID NO:64:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  
GATTAACAAA GATGTACAGA CTGAG 25

(2) INFORMATION FOR SEQ ID NO:65:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:  
GAGACAGCAT TCAGATATAG ACGG 24

(2) INFORMATION FOR SEQ ID NO:66:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
GCGTGGAAATC AAATGGAGTG GC

22

(2) INFORMATION FOR SEQ ID NO:67:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:  
GATGGCCTGT GTGAACAGAT TAAT

24

(2) INFORMATION FOR SEQ ID NO:68:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:  
GAGAGAGATG TCAGAGTCAT TAGC

24

(2) INFORMATION FOR SEQ ID NO:69:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:  
GATCCCCACA ATTTCTTGTG ATTG

24

(2) INFORMATION FOR SEQ ID NO:70:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:  
GTCCCCCTAA AATAATGTGG TAATG

25

(2) INFORMATION FOR SEQ ID NO:71:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:  
GAGGATACTC TCCAATGGTG ATG

23

(2) INFORMATION FOR SEQ ID NO:72:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTCTTAACAT CTAGCCTACT GGAG

24

(2) INFORMATION FOR SEQ ID NO:73:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAGAGGAGCC ATGTATAACAA ACCA

24

(2) INFORMATION FOR SEQ ID NO:74:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCACGCAGGA TCAGATATAG TAATT

26

(2) INFORMATION FOR SEQ ID NO:75:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCTGAAACCT AAGCTGAAGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:76:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTCCCTCACC TCAGATCACCA CC

22

(2) INFORMATION FOR SEQ ID NO:77:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:  
GCTATCTACC TGGCAGGAAA AGAG

24

(2) INFORMATION FOR SEQ ID NO:78:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
GAGTTTCTTA CTATGATCTG GATTC

25

(2) INFORMATION FOR SEQ ID NO:79:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:  
GCAAAATGTA CTCAGCTTCA ATCAC

25

(2) INFORMATION FOR SEQ ID NO:80:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
GTAAAATGCAG TACTGTTCTG ATCC

24

(2) INFORMATION FOR SEQ ID NO:81:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:  
GAATGCTTCA TTCTCATTGT TTAAGG

26

(2) INFORMATION FOR SEQ ID NO:82:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:  
GTCACTAGGA TTCCACAGAA CTTC

24

(2) INFORMATION FOR SEQ ID NO:83:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:  
GAGGTAGGGC TTCCCTTCGC TA

22

(2) INFORMATION FOR SEQ ID NO:84:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:  
GCATAACAAG TGACAGGGTT AGTTA

25

(2) INFORMATION FOR SEQ ID NO:85:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:  
GGTGCTCCTT CCTTACACTG GT

22

(2) INFORMATION FOR SEQ ID NO:86:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:  
GACTACACAT AAACCCACCC CAG

23

(2) INFORMATION FOR SEQ ID NO:87:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
GGGTACAGGA TTTCTAAGAA GTGG

24

(2) INFORMATION FOR SEQ ID NO:88:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
GGAGAAAATT TCAGCTCATC TGAAG

25

(2) INFORMATION FOR SEQ ID NO:89:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(i) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:  
GCTGAAGTTA AGCATTATA CGCC

24

(2) INFORMATION FOR SEQ ID NO:90:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:  
GCGGCTGTAA TGTGCAATGA TGT

23

(2) INFORMATION FOR SEQ ID NO:91:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:  
GACAGCAACC TAATAAACAGC TGTC

24

(2) INFORMATION FOR SEQ ID NO:92:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:  
GTCCTAGGCA CTTGTCACTA GG

22

(2) INFORMATION FOR SEQ ID NO:93:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:  
GAGGGGACTT CCAAGAGTCT CT

22

(2) INFORMATION FOR SEQ ID NO:94:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:  
GTCTTCAGGA AAATTGTAGT TACAG 25

(2) INFORMATION FOR SEQ ID NO:95:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:  
GTTACAAACA CACACGAAGT TCCT 24

(2) INFORMATION FOR SEQ ID NO:96:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
GACTTCCTAA GGCACACTCA GC 22

(2) INFORMATION FOR SEQ ID NO:97:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:  
GTTTAACTAC CTCTCAGGTC ATGA 24

(2) INFORMATION FOR SEQ ID NO:98:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:  
GTCGCCAAGG CTGTAGTGCA AT 22

(2) INFORMATION FOR SEQ ID NO:99:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:  
GAAATAGGTA TCCCTTGATG TCGA

24

(2) INFORMATION FOR SEQ ID NO:100:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:  
GACCAAGAACAT TCAGTTCATC AGTT

24

(2) INFORMATION FOR SEQ ID NO:101:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:  
GAATGAACCA GAGCCAGGAC AG

22

(2) INFORMATION FOR SEQ ID NO:102:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:  
GCCTTGTATG TATGCCGTG CC

22

(2) INFORMATION FOR SEQ ID NO:103:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:  
AAGAGTCCAC CAGGCCATGG A

21

(2) INFORMATION FOR SEQ ID NO:104:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:  
TACCTTGTGT ACTTCTAGCT GAG

23

(2) INFORMATION FOR SEQ ID NO:105:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTTTTTTTTT TTTTTA

17

(2) INFORMATION FOR SEQ ID NO:106:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTTTTTTTTT TTTTTG

17

(2) INFORMATION FOR SEQ ID NO:107:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTTTTTTTTT TTTTTTC

17

(2) INFORMATION FOR SEQ ID NO:108:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGAGTGATG GATATCAA

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(2) INFORMATION FOR SEQ ID NO:109:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGAAAGTGC CAGTGTGCCA TG

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(2) INFORMATION FOR SEQ ID NO:110:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:  
CCCATCACCA TCTTCCAGGA GC

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(2) INFORMATION FOR SEQ ID NO:111:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:  
TTCACCACCT TCTTGATGTC ATCATA

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